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     Oosumi, Chieko; Nozaki, Shinji; Kida, Takao
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CS Ajinomoto Co. Inc., CRL., Kawasaki 210, Japan
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     1998. S131. ISSN: 0032-0781
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AU CASTILLO E M; DE LUMEN B O; REYES P S; DE LUMEN H Z
CS DEP. NUTRITIONAL SCI., UNIV. CALIFORNIA, BERKELEY, CALIF. 94720.
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     Castillo, E.M.; Lumen, B.O. de; Reyes, P.S.; Lumen, H.Z. de
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     Journal of agricultural and food chemistry, Feb 1990. Vol. 38, No.
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    Lumen, Helen Z.
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    Nucleotide sequences for galactinol synthase from zucchini
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    Kerr, Phillip S.; Pearlstein, Richard W.; Schweiger, Bruce J.;
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ANSWER 2 OF 3 CAPLUS COPYRIGHT 1998 ACS

The cDNA for zucchini leaf and soybean seed galactinol synthase (I) are cloned and expressed in a transgenic plant or a host cell using an appropriate regulatory sequence. The plant or plant cell transformed with the cDNA operatively linked to a promoter, e.g., the 35s promoter, may have a varied level of I and thus the desirable levels of raffinose saccharides and sucrose. Nucleotide fragments derived from the cDNA can be used for RFLP breeding of altered levels of raffinose saccharides and sucrose traits in

soybeans. I may also be prepd. in a host, e.g., Escherichia coli, and used for prepg. galactinol.

ANSWER 3 OF 3 WPIDS COPYRIGHT 1998 DERWENT INFORMATION LTD

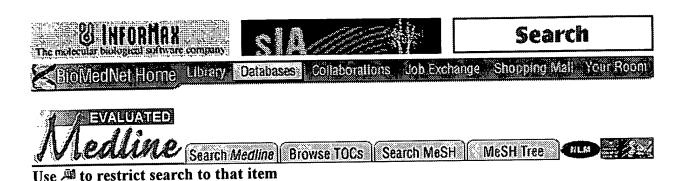
AB WO 9302196 A UPAB: 931119

An isolated pucleic acid fragment (I) comprising a nucleotide

An isolated nucleic acid fragment (I) comprising a nucleotide sequence encoding plant galactinol synthase (GaS) is new.

Also claimed are: (1) a chimeric gene (II) capable of being expressed in transformed plants, comprising (I) operably linked to a suitable regulatory sequence; (2) a chimeric gene (III) capable of being expressed in transformed plants, comprising a nucleic acid fragment encoding antisense RNA complementary to plant GaS; (3) a chimeric gene (IV) capable of being expressed in transformed microorganisms, comprising (I) operably linked to a suitable regulatory sequence; (4) plants transformed with (II) and (III) respectively; (5) seeds obtd. from the plants of (4); (6) a microorganism transformed with (IV); (7) methods for obtaining plants and plant cells contg. altered levels of raffinose saccharides and/or sucrose; (8) 2 methods for producing galactinol; (9) a method of RfLP breeding of altered levels of raffinose saccharides and sucrose traits in soybeans; (10) a method of varying the level of D-galactase contg. oligosaccharides of sucrose in plants in response to end-user requirements.

USE/ADVANTAGE - Transgenic plants that produce higher than normal levels of raffinose saccharides possess enhanced cold tolerance and in coniferous species will result in reduced post harvest needle abscission. Transgenic plants that produce lower than normal levels of raffinose saccharide are more easily digestible and have larger amts. of metabolisable energy. In sugar beets in particular, a decrease in raffinose saccharide content would improve sucrose crystallisation and overcome the need for expensive processing of sugar beet extracts. The enzyme can be used for prodn. of galactinol, and the nucleic acid fragments can be used as RELP markers in soybean genetic studies and breeding programs Dwg.0/3



🍱 Yeast

Volume 8
Issue 2

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IMP2, a nuclear gene controlling the mitochondrial dependence of galactose, maltose and raffinose utilization in Saccharomyces cerevisiae.

Donnini C, Lodi T, Ferrero I, Puglisi PP Yeast 1992 Feb 8:2 83-93

Abstract

The IMP2 gene of Saccharomyces cerevisiae is involved in the nucleo-mitochondrial control of maltose, galactose and raffinose utilization as shown by the inability of imp2 mutants to grow on these carbon sources in respiratory-deficient conditions or in the presence of ethidium bromide and erythromycin. The negative phenotype cannot be scored in the presence of inhibitors of respiration and oxidative phosphorylation, indicating that the role of the mitochondria in the utilization of the above-mentioned carbon sources in imp2 mutants is not at the energetical level. Mutations in the IMP2 gene also confer many phenotypic alterations in respiratory-sufficient conditions, e.g. leaky phenotype on oxidizable carbon sources, sensitivity to heat shock and sporulation deficiency. The IMP2 gene has been cloned, sequenced and disrupted. The phenotype of null imp2 mutants is indistinguishable from that of the originally isolated mutant.

MeSH

Amino Acid Sequence; Base Sequence; Carbohydrates; Galactose; Genes, Fungal; Genetic Complementation Test; Maltose; Mitochondria; Molecular Sequence Data; Mutation; Phenotype; Plasmids; Raffinose; Saccharomyces cerevisiae; Support, Non-U.S. Gov't;

Author Address

Istituto di Genetica, Universita di Parma, Italy.

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BLAST Entrez Nucleotide QUERY Entrez Graphic Other Formats: **FASTA Related Sequences** Protein Links: 24-MAY-1994 BCT 21839 bp DNA **PPSURFOP** LOCUS P.pentosaceus (PPE1.0) sucrose and raffinose operons. DEFINITION Z32771 ACCESSION g493728 NID alpha-galactosidase; alpha-glucosidase; enzyme IIabc; fructokinase; KEYWORDS insertion element; permease; regulator; sucrase. Pediococcus pentosaceus. SOURCE Pediococcus pentosaceus ORGANISM Eubacteria; Firmicutes; Low G+C gram-positive bacteria; Lactobacillaceae; Pediococcus. (bases 1 to 21839) REFERENCE Leenhouts, K.K.J., Bolhuis, A.A., Kok, J.J. and Venema, G.G. **AUTHORS** The sucrose and raffinose operons of Pediococcus pentosaceus PPE1.0 TITLE **JOURNAL** Unpublished (bases 1 to 21839) REFERENCE Leenhouts, K.K. **AUTHORS** Direct Submission TITLE Submitted (27-APR-1994) Leenhouts K. K., Institute for Biological JOURNAL Sciences, Department of Genetics, Kerklaan 30, Haren, The Netherlands, 9751 NN On May 26, 1994 this sequence version replaced gi: 475962. COMMENT Location/Qualifiers FEATURES . 1..21839 source organism="Pediococcus pentosaceus" /strain="PPE1.0" /db_xref="taxon:1255" 487..510 repeat_unit /note="DR2" /citation=[1] /rpt type=DIRECT 488..561 repeat unit /note="IR1" /citation=[1] /rpt_type=INVERTED 513..561 repeat unit /note="DR1" /citation=[1] /rpt type=DIRECT 2724..2760 terminator /standard name="terminator 4" /citation=[1] complement (2929..3864) gene /gene="rafR" complement (2929..3762) CDS /gene="rafR" /standard_name="regulator" /function="regulation raffinose-operon" /citation=[1] /codon start=1 /transl_table=11 /product="regulator" /db xref="PID:g475963" /db_xref="SWISS-PROT:P43465" translation="MNGEYKTLANKSFESNVLFFGQEACLPNYTYKGNNVRDSYVIHY/ IQEGKGTFAAANHPATVLKAGDIFILPKGTPCFYQADNDQPWKYFWIGFSAGIRIEAM LSGSLLAQKCYLRQVQNGHIYADLSELYKVLHIPNSLINDVLLGSLIYRLFYDLLRWY PADATNIKVKSTEQFNLAVSYLQENYSTGCTIMDLCHYLNLSRSYLYTLFKTHANTSP QKLLTKLRLEDAKQRLSTSNNSVQSIANMVGYKDSFTFSKAFKRYSGASPSYYRKSIG

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gene

CDS

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BLAST Entrez **Nucleotide QUERY** NCBI Entrez Other Formats: **FASTA** Graphic Links: Protein **Related Sequences** PDCRAFOPER 21838 bp DNA BCT 23-MAY-1994 LOCUS Pediococcus pentosaceus raffinose operon genes. DEFINITION ACCESSION L32093 q493181 NID agaR gene; agaS gene; agl gene; alpha-galactosidase; KEYWORDS alpha-glucosidase; fructokinase; insertion element; permease; rafP gene; rafR gene; raffinose operon; regulatory protein; scrA gene; scrB gene; scrK gene; scrR gene; sucrase; sucrose-6-phosphate; transport protein. Pediococcus pentosaceus (strain PPE1.0) DNA; Insertion sequence SOURCE IS30 homolog (transposable element Insertion sequence IS30 homolog, kingdom Prokaryotae) DNA; Pediococcus pentosaceus (strain PPE1.0) DNA; Insertion sequence IS3 homolog (transposable element Insertion sequence IS3 homolog, kingdom Prokaryotae) DNA; and Pediococcus pentosaceus (strain PPE1.0) DNA. Pediococcus pentosaceus ORGANISM Eubacteria; Firmicutes; Low G+C gram-positive bacteria; Lactobacillaceae; Pediococcus. (bases 1 to 21838) REFERENCE Leenhouts, K.J., Bolhuis, A.A., Kok, J.J. and Venema, G.G. AUTHORS The sucrose and raffinose operons of Pediococcus pentosaceus PPE1.0 TITLE Unpublished (1994) **JOURNAL** On May 25, 1994 this sequence version replaced gi: 475106. COMMENT Location/Qualifiers **FEATURES** 1..21838 source /organism="Pediococcus pentosaceus" /strain="PPE1.0" /db xref="taxon:1255" repeat unit 487..510 /note="DR2; putative" /rpt type=direct 488..561 repeat unit /note="IR1; putative" /rpt type=inverted 513..561 repeat unit /note="DR1; putative" /rpt type=direct terminator 2724..2760 /standard name="terminator 4" /note="putative" complement (2929..3864) gene /gene="rafR" complement (2929..3762) CDS /gene="rafR" /note="putative" /codon start=1 $/trans\overline{l}_table=11$ /function="regulation raffinose-operon" /product="regulatory protein" /db xref="PID:g475107" /translation="MNGEYKTLANKSFESNVLFFGQEACLPNYTYKGNNVRDSYVIHY IQEGKGTFAAANHPATVLKAGDIFILPKGTPCFYQADNDQPWKYFWIGFSAGIRIEAM LSGSLLAQKCYLRQVQNGHIYADLSELYKVLHIPNSLINDVLLGSLIYRLFYDLLRWY PADATNIKVKSTEQFNLAVSYLQENYSTGCTIMDLCHYLNLSRSYLYTLFKTHANTSP OKLITKIRLEDAKORISTSNNSVQSIANMVGYKDSFTFSKAFKRYSGASPSYYRKSIG complement (3837..3842) -10 signal /gene="rafR"

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- 2221 tagataaatt aattataaaa COCOO	dadaa taaattitti cyayaaaaay gaattaaaa
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Other Formats:

Links:

LOCUS

ECORA

BLAST Entrez Nucleotide QUERY NCBI Entrez Graphic **FASTA** Other Formats: Related Sequences MEDLINE Protein 15-JUN-1990 BCT DNA **ECORAF** 5284 bp LOCUS E.coli rafA, rafB, and rafD genes encoding alpha-D-galactosidase, DEFINITION raf-permease, and raf-invertase, complete cds. ACCESSION M27273 g147504 NID alpha-D-galactosidase; raf-invertase; raf-permease; rafA gene; rafB **KEYWORDS** gene; rafD gene. E.coli (strain K-12) DNA. SOURCE ORGANISM Escherichia coli Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia. (bases 1 to 5284) REFERENCE Aslanidis, C., Schmid, K. and Schmitt, R. **AUTHORS** Nucleotide sequences and operon structure of plasmid-borne genes TITLE mediating uptake and utilization of raffinose in Escherichia coli J. Bacteriol. 171, 6753-6763 (1989) JOURNAL 90078124 MEDLINE Draft entry and computer readable copy of sequence [1] kindly COMMENT provided by R.Schmitt, 01-SEP-1989. Location/Qualifiers **FEATURES** 1..5284 source /organism="Escherichia coli" /db xref="taxon:562" 12..17 -35 signal 36..41 -10 signal 58..63 RBS /note="S.D. sequence (ribosome binding site)" CDS 70..2196 /note="alpha-D-galactosidase" /codon_start=1 /transl table=11 /db $xre\overline{f}="PID:\overline{g1}47505"$ translation="MISKYCRLSSPRSDLIIKTHPHAEIIWWGSALKHFSPDDCASLE/ RPVANGRLDIDTPLTLIAENALGLFSSPGLEGHRNGLDASPVFYTVDVEHTENTLRLT SEDSVAGLRLVSELVMTPSGILKVRHALTNLREGDWQINRFAITLPVAERAEEVMAFH GRWTREFQPHRVRLTHDAFVLENRRGRTSHEHFPALIVGTPGFSEQQGEVWAVHLGWS GNHRMRCEAKTDGRRYVQAEALWMPGEKALRKNETLYTPWLYACHSADGLNGMSQQYH RFLRDEIIRFPEQKLRPVHLNTWEGIYFNHNPDYIMQMAERAAALGVERFIIDDGWFK GRNDDRAALGDWYTDEQKYPNGLMPVINHVKSLGMEFGIWVEPEMINPDSDLFRLHPD WILSMPGYSQPTGRYQYVLNLNIPEAFDYIYKRFLWLLGEHPVDYVKWDMNRELVQAG HEGRAAADAQTRQFYRLLDLLRERFPHVEFESCASGGGRIDFEVLKRTHRFWASDNND ALERCTIQRGMSYFFPPEVMGAHIGHRRCHATFRQHSIAFRGLTALFGHMGLELDPVA ADAKESDGYRRYALLYKEWRQLIHTGVLWRVDMPDSSIQVQGVVSPDQSQALFMISQL AMPDYTLPGILRFPGLAAEVRYRLRVIDHPEIQLVGEGGHTMRRLPAWMNQPLEASGE WLAKGGIQLPVLDPESAILIALERAV" 2244..2249 RBS /note="S.D. sequence (ribosome binding site)" 2259..3536 CDS /note="raf-permease" /codon start=1 /trans $\overline{1}$ _table=11 /db_xref="PID:g147506" /translation="MNSASTHKNTDFWIFGLFFFLYFFIMATCFPFLPVWLSDVVGLS ${ t KTDTGIVFSCLSLFAISFQPLLGVISDRLGLKKNLIWSISLLLVFFAPFFLYVFAPLL}$ HLNIWAGALTGGVFIGFVFSAGAGAIEAYIERVSRSSGFEYGKARMFGCLGWALCATM AGILFNVDPSLVFWMGSGGALLLLLLLYLARPSTSQTAMVMNALGANSSLISTRMVFS LFRMRQMWMFVLYTIGVACVYDVFDQQFAIFFRSFFDTPQAGIKAFGFATTAGEICNA IIMFCTPWIINRIGAKNTLLVAGGIMTIRITGSAFATTMTEVVILKMLHALEVPFLLV

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